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# 2

## RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/081,280

TIME: 09:29:40

Input Set : N:\Crf3\RULE60\10081280.raw

Output Set: N:\CRF3\03262002\J081280.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

7 (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

9 (iii) NUMBER OF SEQUENCES: 11

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Genentech, Inc.

13 (B) STREET: 460 Point San Bruno Blvd

14 (C) CITY: South San Francisco

15 (D) STATE: California

16 (E) COUNTRY: USA

17 (F) ZIP: 94080

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

C--&gt; 26 (A) APPLICATION NUMBER: US/10/081,280

--&gt; 27 (B) FILING DATE: 21-Feb-2002

28 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/829,270

33 (B) FILING DATE: 31-Mar-1997

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Marschang, Diane L.

38 (B) REGISTRATION NUMBER: 35,600

39 (C) REFERENCE/DOCKET NUMBER: P1007R1

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415/225-5416

43 (B) TELEFAX: 415/952-9881

44 (C) TELEX: 910/371-7168

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 181 amino acids

50 (B) TYPE: Amino Acid

51 (D) TOPOLOGY: Linear

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

56 1 5 10 15

58 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser

59 20 25 30

61 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu

ENTERED

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Input Set : N:\Crf3\RULE60\10081280.raw

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62	35	40	45
64	Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro		
65	50	55	60
67	Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln		
68	65	70	75
70	Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala		
71	80	85	90
73	Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu		
74	95	100	105
76	Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly		
77	110	115	120
79	Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro		
80	125	130	135
82	Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His		
83	140	145	150
85	Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys		
86	155	160	165
88	Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro		
89	170	175	180
91	Thr		
92	181		

## 94 (2) INFORMATION FOR SEQ ID NO: 2:

## 96 (i) SEQUENCE CHARACTERISTICS:

97 (A) LENGTH: 433 base pairs

98 (B) TYPE: Nucleic Acid

99 (C) STRANDEDNESS: Single

100 (D) TOPOLOGY: Linear

## 102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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105 CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
107 TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100
109 CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150
111 ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200
113 TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
115 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
117 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
119 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
121 ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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## 123 (2) INFORMATION FOR SEQ ID NO: 3:

## 125 (i) SEQUENCE CHARACTERISTICS:

126 (A) LENGTH: 28 base pairs

127 (B) TYPE: Nucleic Acid

128 (C) STRANDEDNESS: Single

129 (D) TOPOLOGY: Linear

## 131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

134 CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

## 136 (2) INFORMATION FOR SEQ ID NO: 4:

## 138 (i) SEQUENCE CHARACTERISTICS:

139 (A) LENGTH: 28 base pairs

140 (B) TYPE: Nucleic Acid

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141         (C) STRANDEDNESS: Single
142         (D) TOPOLOGY: Linear
144         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
147 CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28
149 (2) INFORMATION FOR SEQ ID NO: 5:
151     (i) SEQUENCE CHARACTERISTICS:
152         (A) LENGTH: 1438 base pairs
153         (B) TYPE: Nucleic Acid
154         (C) STRANDEDNESS: Single
155         (D) TOPOLOGY: Linear
157     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
160 GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
162 TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
164 AGCTCATATCC TGTGCCCCTG GTCGACGACG GCAGCCCAGC GCTTCGCGTG 150
166 TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
168 CAGAGGGGGC ACCTGGTCCG ACTCGGTTGG GCTCGGGCGG CCCCCTGCC 250
170 CCCCCTGGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
172 GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
174 AGCCCCTGGG GCGCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
176 GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCCA 450
178 GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
180 AGATTGGTCT GTTTTGTGTC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
182 GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCA 600
184 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCGCT 650
186 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
188 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
190 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
192 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
194 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
196 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
198 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
200 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
202 GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
204 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150
206 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTGTCA CTTACACAGA 1200
208 GAGTCACATT GATATAGCTT TAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
210 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
212 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
214 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
216 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438
218 (2) INFORMATION FOR SEQ ID NO: 6:
220     (i) SEQUENCE CHARACTERISTICS:
221         (A) LENGTH: 417 amino acids
222         (B) TYPE: Amino Acid
223         (D) TOPOLOGY: Linear
225     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
227 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
228 1          5          10          15
230 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser

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231		20		25		30
233	Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu					
234		35		40		45
236	Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro					
237		50		55		60
239	Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln					
240		65		70		75
242	Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala					
243		80		85		90
245	Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu					
246		95		100		105
248	Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly					
249		110		115		120
251	Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro					
252		125		130		135
254	Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His					
255		140		145		150
257	Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys					
258		155		160		165
260	Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro					
261		170		175		180
263	Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys					
264		185		190		195
266	Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu					
267		200		205		210
269	Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg					
270		215		220		225
272	His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly					
273		230		235		240
275	Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu					
276		245		250		255
278	Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys					
279		260		265		270
281	Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr					
282		275		280		285
284	Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp					
285		290		295		300
287	Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr					
288		305		310		315
290	Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln					
291		320		325		330
293	Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg					
294		335		340		345
296	Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu					
297		350		355		360
299	Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln					
300		365		370		375
302	Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu					
303		380		385		390

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305 Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
306                               395                               400                               405
308 Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
309                               410                               415                               417
311 (2) INFORMATION FOR SEQ ID NO: 7:
313     (i) SEQUENCE CHARACTERISTICS:
314         (A) LENGTH: 27 base pairs
315         (B) TYPE: Nucleic Acid
316         (C) STRANDEDNESS: Single
317         (D) TOPOLOGY: Linear
319     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
322 GGCGCTCTGG TGGCCCTTGC AGAAGCC 27
324 (2) INFORMATION FOR SEQ ID NO: 8:
326     (i) SEQUENCE CHARACTERISTICS:
327         (A) LENGTH: 25 base pairs
328         (B) TYPE: Nucleic Acid
329         (C) STRANDEDNESS: Single
330         (D) TOPOLOGY: Linear
332     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
335 TTCGGCCGAG AAGTTGAGAA ATGTC 25
337 (2) INFORMATION FOR SEQ ID NO: 9:
339     (i) SEQUENCE CHARACTERISTICS:
340         (A) LENGTH: 1634 base pairs
341         (B) TYPE: Nucleic Acid
342         (C) STRANDEDNESS: Single
343         (D) TOPOLOGY: Linear
345     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
348 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACACGACG GGCAGAGAGC 50
350 ACGGAGCCCG GAAGCCCCTG GCGGCCCGTC GGAGGGCT   ATG GAG 94
351                                     Met Glu
352                                     1
354 CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
355 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
356     5                               10                               15
358 CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
359 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
360     20                               25
362 CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
363 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
364     30                               35                               40
366 AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
367 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
368     45                               50
370 CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
371 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
372     55                               60                               65
374 TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
375 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
376     70                               75                               80

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VERIFICATION SUMMARY

DATE: 03/26/2002

PATENT APPLICATION: US/10/081,280

TIME: 09:29:41

Input Set : N:\Crf3\RULE60\10081280.raw

Output Set: N:\CRF3\03262002\J081280.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9